Objectives
Microbial communities greatly contribute to this key process by expressing a suite of various extracellular and intracellular enzymes. However, the key players and the details of the nitrogen flux is widely unknown. Protein-SIP combine classical metaproteomics with functional information resulting from isotope incorporation into proteins thus allows tracking nutrient flux within degrading communities (Taubert et al., ISME 2012).

Materials and Methods
Soil from a tobacco field in Germany was properly mixed with leaf litter from either ^{15}N-labeled tobacco or ^{13}C-labeled corn plants as substrate. Sampling took place 7 times within two week experiments and 9 times within a 14 week experiment. Protein lysates were separated by 1-D-SDS-PAGE followed by liquid-chromatography and tandem mass-spectrometry. Mass spectra were assigned using a metagenome sequence database.

Results
10,100 distinct peptides were identified in the ^{15}N tobacco litter experiment to which the metagenome contributed to about 30%. Besides energy conversion/production and carbohydrate/amino acid metabolism, cell envelope biogenesis/outer membrane were the functional groups of major relevance. In addition, several groups of microbial groups were identified to have different metabolic impacts on leaf litter degradation. *Pseudomonadales* and *Xanthomonadales* showed highest metabolic activity towards the leaf litter. *Burkholderiales* and Bacteroidetes revealed moderate metabolic. In contrast, members belonging to *Actinomycetales* and *Rhizobiales* showed only low degradation activity.

Conclusion
Our study revealed a link of phylogenetic origin and functional information to during nutrient cycling based proteins and provides a deep insight into molecular details of the leaf-litter decomposition process.

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Population genomics of the legume plant host specific selection of rhizobial genotypes

B. Jorrín[1], J. Imperial[1]
[1]Centro de Biotecnología y Genómica de Plantas (UPM-INIA), Pozuelo de Alarcón, Spain

Introduction
Rhizobium leguminosarum bv. viciae (*Rlv*) establish effective symbioses with four legume genera: *Pisum*, *Lens*, *Lathyrus* and *Vicia*. Classic studies using trap plants provided evidence that, given a choice, specific hosts select specific genotypes of rhizobia which are, apparently, particularly adapted to that host (Mutch & Young, 2004; Louvrier et al, 1996).

Objective
Pooled DNA samples from *Rlv* nodule isolates obtained from different legume plant hosts used as rhizobial traps should allow a test of the hypothesis that different plant hosts select specific subpopulations of rhizobia from the available population present in a given soil.

Materials and Methods
We have applied a Pool-Seq approach (Kofler et al, 2011), to study plant host selection of genotypes from the available rhizobial genomic diversity present in a well-characterized agricultural soil (INRA Bretennieres). Plants of *P. sativum*, *L. culinaris*, *V. sativa* and *V. faba* were employed as traps. We pooled 100 nodule isolates from each host, and the pooled DNAs were sequenced (BGI-Hong Kong; Illumina Hi-Seq 2000, 180 bp PE libraries, 100 bp reads, 12 Mreads). Reads were quality filtered with Trimmomatic, mapped with Bowtie2 using Rlv 3841 as reference genome. Single Nucleotide Polymorphisms (SNPs) were called with VarScan. Results were visualized with SeqMonk and IGV.

Results
Our results confirm, at the genomic level, previous observations regarding plant selection of specific genotypes. We expect that further, ongoing comparative studies on differential Pool-Seq sequences will identify specific gene components of the plant-selected genotypes.

Conclusions
Since rhizobial populations are a minor fraction of the soil microbiota, any attempt to approach the genomic structure of such populations will necessarily require a preliminary enrichment through the use of legume host trap plants, thus potentially introducing a host-mediated bias.

Our work discussed here provides genomic evidence that specific hosts select specific genotypes from the available variability present in the soil.

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References
Mutch LA & Young JP 2004 Mol Ecol 13: 2435
Louvrier P et al 1996 Appl Environ Microbiol 62:4202
Kofler R et al 2011 Bioinformatics 27:3435-3436

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Soil microbial community structure and function in relation to water regime changes in the Namib Desert

A. Frossard[1], E. Gunnigle[1], J.- B. Ramond[1], M. Seely[2], D. Cowan[1]
[1]University of Pretoria, Centre for Microbial Ecology and Genomics/ Genetics, Pretoria, South Africa
[2]Gobabeb Training and Research and Centre, Gobabeb, Namibia

Arid systems constitute the most extensive and one of the harshest terrestrial biome on earth. Contrastingly, their microbial community structure and function dynamics remain largely unknown. In this environment, microbial metabolism is strongly affected by water availability (e.g. timing, intensity and frequency of water pulse events) and is expected to vary diurnally in relation with soil moisture levels and temperature. We aimed to evaluate and determine factors driving the dynamics of desert soil microbial community structures and functions using a combination of molecular tools (16S rRNA gene T-RFLP), ecophysiological methods (enzyme assays) and environmental measurements (soil chemical parameters). *In situ* and controlled microcosm experiments were performed to evaluate the impact of (i) soil moisture and temperature variation during diurnal cycles and (ii) distinct water pulses on microbial community structure and functions. In a field study in the Namib Desert, we sampled a single site over a 5 day period, 3 times per day (early morning, midday and night) to reflect diurnal cycles. Soil surface temperature and moisture were recorded during the entire sampling period. In a